FIG. 1A

```
tacacggccg cagctgaaca gcatcaccgc tgtcccaagg acaaccccaa agaggggcct 60

cgactgcacc tcctcgaagt tgctggctgg ctttggcaag tgcaggaatg gtgttttgtg 120

agggcatgga tggagaagtg ccaagggccc ctgtttggtc acttccgaag agcaaaaacg 180

tgttgagagg agaccggttt aagatttcaa acagaacctc cccagcgcgc atgaaaggac 240

ttgattagca tatgtcaaga ggacccgctt atatactcgg tgtgtatgta cacaggactc 300

tgatctgatc agtttgcgga attggagccc cagccaacag ccctagtcct agtattggca 360

gcggcagcta tagatatttc tgcagagcca gcagccggct cccacctacc caaggagaga 420

agatcgctcc aagacagtga gagcttccct gccatttcag tgcaaagtcc ctccggagcg 480

acctcagagg agtaaccggg ccttaacttt ttgcgctcgt tttgctataa tttttctcta 540

tccacctcca tcccaccccc acaacactct ttactggggg ggtcttttgt gttccggatc 600

tccccctcc atg gct ccc tta gcc gaa gtc ggg ggc ttt ctg ggc ggc ctg 651
          Met Ala Pro Leu Ala Glu Val Gly Gly Phe Leu Gly Gly Leu
            1               5                  10

gag ggc ttg ggc cag cag gtg ggt tcg cat ttc ctg ttg cct cct gcc   699
Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala
 15                  20                  25                  30

ggg gag cgg ccg ccg ctg ctg ggc gag cgc agg agc gcg gcg gag cgg   747
Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg
                 35                  40                  45

agc gcc cgc ggc ggg ccg ggg gct gcg cag ctg gcg cac ctg cac ggc   795
Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly
             50                  55                  60

atc ctg cgc cgc cgg cag ctc tat tgc cgc acc ggc ttc cac ctg cag   843
Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln
         65                  70                  75

atc ctg ccc gac ggc agc gtg cag ggc acc cgg cag gac cac agc ctc   891
Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu
     80                  85                  90

ttc ggt atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att   939
Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile
 95                 100                 105                 110

aga ggt gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa   987
Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu
                115                 120                 125
```

FIG. 1B

```
ctc tat gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag     1035
Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln
            130                 135                 140

ttt gaa gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat     1083
Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His
        145                 150                 155

gga gac act ggc cgc agg tat ttt gtg gca ctt aac aaa gac gga act     1131
Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr
    160                 165                 170

cca aga gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc     1179
Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe
175                 180                 185                 190

tta cct aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag gac     1227
Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp
                195                 200                 205

cta ctg atg tac act tga agtgcgatag tgacattatg gaagagtcaa           1275
Leu Leu Met Tyr Thr
            210

accacaacca ttctttcttg tcatagttcc catcataaaa taatgaccca agcag       1330
```

FIG. 2

```
  1 MAPLAEVGGFLGGLEGLGQQVGSHFLLPPAGERPPLLGERRSAAERSA.R 49
    |||| ||| : |  : .    |.  .||   : | || :    .|
  1 MAPLGEVGNYFGVQDAV..PFGNVPVLPV..DSPVLLSDHLGQSEAGGLP 46

 50 GGPGAAQLAHLHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILE 99
     ||    | || |||||||||||||||:| |.|.:||||.||| |||||
 47 RGPAVTDLDHLKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILE 96

100 FISVAVGLVSIRGVDSGLYLGMNDKGELYGSEKLTSECIFREQFEENWYN 149
    |||:||||||||||||||||||:|||||||||| ||:||||||||||
 97 FISIAVGLVSIRGVDSGLYLGMNEKGELYGSEKLTQECVFREQFEENWYN 146

150 TYSSNIYKHGDTGRRYFVALNKDGTPRDGARSKRHQKFTHFLPRPVDPER 199
    |||||:||| ||||||:||||||||||:| |.||||||||||||||::
147 TYSSNLYKHVDTGRRYYVALNKDGTPREGTRTKRHQKFTHFLPRPVDPDK 196

200 VPELYKDLLMYT 211
    |||||||:|  .
197 VPELYKDILSQS 208
```

FIG. 3

```
  1 MAPLAEVGGFLGGLEGLGQQVGSHFLLPPAGERPPLLGERRSAAERSA.R 49
    |||| ||| : |  : .    |.  .||   : | || :    .|
  1 MAPLGEVGSYFGVQDAV..PFGNVPVLPV..DSPVLLSDHLGQSEAGGLP 46

 50 GGPGAAQLAHLHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILE 99
     ||    | || |||||||||||||||:| |.|.:||||.||| |||||
 47 RGPAVTDLDHLKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILE 96

100 FISVAVGLVSIRGVDSGLYLGMNDKGELYGSEKLTSECIFREQFEENWYN 149
    |||:||||||||||||||||||:|||||||||| ||:||||||||||
 97 FISIAVGLVSIRGVDSGLYLGMNEKGELYGSEKLTQECVFREQFEENWYN 146

150 TYSSNIYKHGDTGRRYFVALNKDGTPRDGARSKRHQKFTHFLPRPVDPER 199
    |||||:||| ||||||:||||||||||:| |.||||||||||||||::
147 TYSSNLYKHVDTGRRYYVALNKDGTPREGTRTKRHQKFTHFLPRPVDPDK 196

200 VPELYKDLLMYT 211
    |||||||:|  .
197 VPELYKDILSQS 208
```

FIG. 4

```
hu FGF-9    MAPLGEVGNY FGVQDAV..P FGNVPVLPV. .DSPVLLSDH LGQSEAGGLP RGPAVTDLDH
hu FGF-16   MA...EVGGV FASLDWDLHG FSSSLGNVPL ADSPGFLNER LGQIE.GKLQ RGSP.TDFAH
hu FGF-L    MAPLAEVGGF LGGLEGLGQQ VGSHFLLPPA GERPPLLGER RSAAERSA.R GGPGAAQLAH
mu FGF-9    MAPLGEVGSY FGVQDAV..P FGNVPVLPV. .DSPVLLNDH LGQSEAGGLP RGPAVTDLDH
ra FGF-16   MA...EVGGV FASLDWDLQG FSSSLGNVPL ADSPGFLNER LGQIE.GKLQ RGSP.TDFAH

hu FGF-9    LKGILRRRQL YCRTGFHLEI FPNGTIQGTR KDHSRFGILE FISIAVGLVS IRGVDSGLYL
hu FGF-16   LKGILRRRQL YCRTGFHLEI FPNGTVHGTR HDHSRFGILE FISLAVGLIS IRGVDSGLYL
hu FGF-L    LHGILRRRQL YCRTGFHLQI LPDGSVQGTR QDHSLFGILE FISVAVGLVS IRGVDSGLYL
mu FGF-9    LKGILRRRQL YCRTGFHLEI FPNGTIQGTR KDHSRFGILE FISIAVGLVS IRGVDSGLYL
ra FGF-16   LKGILRRRQL YCRTGFHLEI FPNGTVHGTR HDHSRFGILE FISLAVGLIS IRGVDSGLYL

hu FGF-9    GMNEKGELYG SEKLTQECVF REQFEENWYN TYSSNLYKHV DTGRRYYVAL NKDGTPREGT
hu FGF-16   GMNERGELYG SKKLTRECVF REQFEENWYN TYASTLYKHS DSERQYYVAL NKDGSPREGY
hu FGF-L    GMNDKGELYG SEKLTSECIF REQFEENWYN TYSSNIYKHG DTGRRYFVAL NKDGTPRDGA
mu FGF-9    GMNEKGELYG SEKLTQECVF REQFEENWYN TYSSNLYKHV DTGRRYYVAL NKDGTPREGT
ra FGF-16   GMNERGELFG SKKLTRECVF REQFEENWYN TYASTLYKHS DSERQYYVAL NKDGSPREGY

hu FGF-9    RTKRHQKFTH FLPRPVDPDK VPELYKDILS QS
hu FGF-16   RTKRHQKFTH FLPRPVDPSK LPSMSRDLFH YR
hu FGF-L    RSKRHQKFTH FLPRPVDPER VPELYKDLLM YT
mu FGF-9    RTKRHQKFTH FLPRPVDPDK VPELYKDILS QS
ra FGF-16   RTKRHQKFTH FLPRPVDPSK LPSMSRDLFR YR
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